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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:18:03 ; Search time 1460.69 Seconds
(without alignment)
12007.805 Million cell updates/sec

Title: US-09-807-933B-6

Perfect score: 1083
Sequence: 1 atgaagttccttaccattgc.....ctggctgtccaagaataa 1083

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 33308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estinu:*
4: em_estov:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	179	16.5	691	10 BE585661 EST#6PSP6
2	146.2	13.5	450	13 BI200722 BI200722
3	128.6	11.9	444	13 BI190695 BI190695
4	122.2	11.3	426	13 BI187295 BI187295
5	86	7.9	215	13 BI190568 BI190568
6	85.6	7.9	619	17 FR0047601 AL444386 Fugu rubr

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BE585661	691 bp	EST#6PSP6 D02_d2_014 KSU wheat Fusarium graminearum infected spike	BE585661	1	GI:9838604	bread wheat.	Triticum aestivum	EST#6PSP6 D02_d2_014 KSU wheat Fusarium graminearum infected spike	Matthews, A. and Gill, B.S.	The structure and function of the expressed portion of the wheat genomes - Kansas State University, Fusarium graminearum infected spike cDNA library	unpublished (2000)	Contact: John Fellers US Department of Agriculture, Agriculture Research Service, Plant Science and Entomology Unit Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State University, Manhattan, KS 66506, USA Tel: 785-532-2367 Fax: 785-532-6167 Email: jpf@alfalfa.ksu.edu

ALIGNMENTS

BE585661 691 bp mRNA linear EST 17-AUG-2000
EST#6PSP6 D02_d2_014 KSU wheat Fusarium graminearum infected spike
cDNA library Triticum aestivum CDNA clone EST#6PSP6_D02_d2_014,
mRNA sequence.
BE585661.1 GI:9838604
EST.
bread wheat.
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticaceae; Triticum.
1 (bases 1 to 691)
Fellers, J.P., Li, W.L., Hill-Ambroz, K., Matthews, A. and Gill, B.S.
The structure and function of the expressed portion of the wheat
genomes - Kansas State University, Fusarium graminearum infected
spike cDNA library
unpublished (2000)
Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
Tel: 785-532-2367
Fax: 785-532-6167
Email: jpf@alfalfa.ksu.edu
Sequence have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20
Seq primer: SP6.

FEATURES
Location/Qualifiers
source

1..691
/organism="Triticum aestivum"
/cultivar="Sumai3"
/db_xref="taxon:4565"
/clone="ESTH6PSP6 D02 d2 014"
/clone_1ib="KSU wheat Fusarium graminearum infected spike
cDNA library"
/issue_type="Spike"
/dev_stage="Adult Plant"
/lab_host="E. coli JM109"
/note="Vector: pGEM-T easy; Site 1: SacII; Site 2: SpeI;
plants were grown in the greenhouse. Spikes were sprayed
with Fusarium graminearum (at what stage). Total RNA, and
poly(A) RNA were prepared from infected spikes. cDNA was
prepared using the SmartTM PCR cDNA synthesis kit from
Clontech. cDNA was cloned into the pGEM-T easy vector
from Promega."

BASE COUNT 135 a 196 c 163 g 197 t

Query Match 16.5%; Score 179; DB 10; Length 691;
Best Local Similarity 65.5%; Pred. No. 5.7e-36;
Matches 298; Conservative 0; Mismatches 145; Indels 12; Gaps 2;

449 GTGGTGCCTCCGGATATGTGTAACCACTGCTACTGAGGATTTGTGTAAGCTTTCTTGA 508
160 GTGCTGCTTCTGGAAGGTGCACTGATCTGAGCTGCTCAAGCCCTTCTTGT 219
509 GTTGGCCCGGTAAAGCTGATGTCACCTCCCTGTTGGCTCTGTAAAGATGTAGA 568
220 CTGGAGATGGCAAGCCAAAGTGCAGCCCTGCTTTGACTTGTGACAAAAAGACAAC 279
569 CTCTTGCATTAACAACACTCAAAACGCGTGTG---TTGGTGTAGACAGTACACTGTA 625
280 CCACTACTACCTGAACCCCGTCAACGGTTGTGAGAGTGGTGTGCTTTGCTTGTGA 339
626 ATGACATCAACCTTGGTGTGACGACACCTTGGCTTGGCTTGGCGCTTCCA 685
340 CTAATCTACCTCCCTGGGCTGTCAACGACCTTGTGAGGTTTACCTGCTACCAAGC 399
686 TTTCTGGTGTAGGCAAGCTACTGTTGTGCTGTTTGAACCTACATCACTCTTA 745
400 TTGCTGGTGGCACTGACACAGCTGTGTGTGTATGCTCTACCTTACGACCG 459
746 CTGCGGTCAAGGGTAAAGATGTTGTTCAAGTACCAACACTGTGTTGACCTTGGCT 805
460 GTCCCGTAAAGGAAAGATGATGTTGTCAGTCCACCAACACTGTGTGTGATCTCGGTG 519
806 CTAACTGCTGTCTGCTTGAAGTCCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 865
520 ATAAAC-----CACTTGAACCTTATGATCCCGCGGTGTGTGTGTGTGTGTGTGTGT 570
866 GTTGTGCACTCAATGAGGTGTCTCCACCGATGT 900
571 GATGCACTCTGATGTTCCGCAAGCCCTCGTGTGT 605

RESULT 2
BI200729 450 bp mRNA linear EST 10-JUL-2001
LOCUS BI200729
DEFINITION library Fusarium sporotrichioides Tri 10 overexpressed cDNA
1library Fusarium sporotrichioides cDNA clone o1f05ts 5', mRNA

ACCESSION BI200729
VERSION BI200729.1 GI:14666701
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 450)
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand
M., and Roe, B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
CONTACT: Bruce A. Roe, University of Oklahoma, broeou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broeou.edu

Contract Dr. Marian Beremand regarding clone availability. Included
is the best homolog from a blastx search of Genbank nr 04-09-01
633 5e-66 gi|1170140|sp|P45699 POTATIVE ENDONUCLEASE TYPE
KREBUNSOR EN
Seq primer: T3
High quality sequence stop: 440.
Location/Qualifiers
1..450
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone_1ib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 90 a 125 c 102 g 133 t

Query Match 13.5%; Score 146.2; DB 13; Length 450;
Best Local Similarity 67.6%; Pred. No. 1.8e-27;
Matches 221; Conservative 0; Mismatches 103; Indels 3; Gaps 1;

449 GTGGTGCCTCCGGATATGTGTAACCACTGCTACTGAGGATTTGTGTAAGCTTTCTTGA 508
124 GTGCTGCTTCTGGAAGGTGCACTGATCTGAGCTGCTCAAGCCCTTCTTGT 183
509 GTTGGCCCGGTAAAGCTGATGTCACCTCCCTGTTGGCTCTGTAAAGATGTAGA 568
184 CTGGAGATGGCAAGCCAAAGTGCAGCCCTGCTTTGACTTGTGACAAAAAGACAAC 243
569 CTCTTGCATTAACAACACTCAAAACGCGTGTG---GTGGTGTAGACAGTACACTGTA 625
244 CTAATCTACCTGAACCCCGTCAACGGTTGTGAGAGTGGTGTGCTTATGCTTGA 303
626 ATGACATCAACCTTGGTGTGACGACACCTTGGCTTGGCTTGGCGCTTCCA 685
304 CCACTACTCCCGGGGCTGTCAACGACCTTGTGAGGTTTGCCTGCTACCAAGC 363
686 TTTCTGGTGTAGGCAAGCTACTGTTGTGCTGTTTGAACCTACATCACTCTTA 745
364 TTGCTGGTGGCACTGACACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 423
746 CTGCGGTCAAGGGTAAAGATGTTG 772
424 GTCCCGTAAAGGCAAGATGATG 450

RESULT 3
BI190695 444 bp mRNA linear EST 10-JUL-2001
LOCUS BI190695
DEFINITION library Fusarium sporotrichioides Tri 10 overexpressed cDNA
1library Fusarium sporotrichioides cDNA clone 13g10fs 5', mRNA

ACCESSION BI190695
VERSION BI190695.1 GI:14664374
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Hypocreales; microsporitic Hypocreales; Fusarium.
1 (bases 1 to 444)
Ren.O., Tag.A., Peplow.A., Lai.H., Kupfer.C., Peterson.A., Beremand
M. and Roe.B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability. Included
is the best homolog from a blastx search of Genbank nr 04-09-01
576 3e-59 g11170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
KRECURSOR (EN
Seq primer: T3.

FEATURES
source

1..444
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="1391018"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT
ORIGIN

85 a 127 c 92 g 140 t

Query Match 11.3%; Score 128.6; DB 13; Length 444;
Best Local Similarity 67.1%; Pred. No. 7.1e-23;
Matches 198; Conservative 0; Mismatches 94; Indels 3; Gaps 1;

449 GTGTGCTCCGGTAATGTAAGTAACCACTGCTACTGGATTTGTAAGCTTTCTTGA 508
150 GTGTGCTTCTGGAAGTGGCACTCTACTGATCTGGAGCTGCGAAGCTTTCTTCT 209
509 GTTGGCCGGTAAGGCTGATGTACCTCCCTGTTGGCTCTGTACAAGATGTAGA 568
210 CTGGAGGGGGAAGGCTAAAGTCAAGCGCCCTGCTGACTGTGACAAAGATAACC 269
569 CTCTTGCATTAACAACACTGAACGGCTGT---GTTGGTGTAGACAGCTACACTTA 625
270 CTATCACTAACCTGAACGCTGTCAACGGTGTGAGGGTGTCTGCTTATGCTTGA 329
626 ATGACAATCAACTTGGGTTGTTAGCGACGACCTTGCCTTACGCTTCCGCTTCCA 685
330 CCAACTACTCCCGTGGGCTGTCAACGACGACCTTGCCTTACGCTTCCGCTTCCA 389
686 TTCTGTGTGAGGGAAGCTACTTGTGTTGCTGCTTTGCAACTACATTTCAC 740
390 TTGCTGTGTGTAGTAGGCGACGCTGTGCTGTGCTTGAAGCTCTACCTTCAC 444

RESULT 4
BI187295
LOCUS
DEFINITION

426 bp mRNA linear EST 10-JUL-2001
BI187295
1library Fusarium sporotrichioides cDNA clone ah11fs 5', mRNA
sequence.
BI187295
BI187295.1 GI:14660974
EST.
Fusarium sporotrichioides.
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; microsporitic Hypocreales; Fusarium.
1 (bases 1 to 426)
Ren.O., Tag.A., Peplow.A., Lai.H., Kupfer.C., Peterson.A., Beremand
M. and Roe.B.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

BI187295
BI187295.1
EST.
Fusarium sporotrichioides.
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; microsporitic Hypocreales; Fusarium.
1 (bases 1 to 426)
Ren.O., Tag.A., Peplow.A., Lai.H., Kupfer.C., Peterson.A., Beremand
M. and Roe.B.

TITLE
JOURNAL
COMMENT

Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Other ESTs: ah11fs.fl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability. Included
is the best homolog from a blastx search of Genbank nr 04-09-01
565 5e-58 g11170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
KRECURSOR (EN
Seq primer: T3
High quality sequence stop: 338.

FEATURES
source

1..426
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="ah11fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT
ORIGIN

82 a 119 c 91 g 134 t

Query Match 11.3%; Score 122.2; DB 13; Length 426;
Best Local Similarity 66.6%; Pred. No. 3.3e-21;
Matches 191; Conservative 0; Mismatches 93; Indels -3; Gaps 1;

449 GTGTGCTCCGGTAATGTAAGTAACCACTGCTACTGGATTTGTAAGCTTTCTTGA 508
140 GTGTGCTTCTGGAAGTGGCACTCTACTGATCTGGAGCTGCGAAGCTTTCTTCT 199
509 GTTGGCCGGTAAGGCTGATGTACCTCCCTGTTGGCTCTGTACAAGATGTAGA 568
200 CTGGAGGGGGAAGGCTAAAGTCAAGCGCCCTGCTGACTGTGACAAAGATAACC 259
569 CTCTTGCATTAACAACACTGAACGGCTGT---GTTGGTGTAGACAGCTACACTTA 625
260 CTATCACTAACCTGAACGCTGTCAACGGTGTGAGGGTGTCTGCTTATGCTTGA 319
626 ATGACAATCAACTTGGGTTGTTAGCGACGACCTTGCCTTACGCTTCCGCTTCCA 685
320 CCAACTACTCCCGTGGGCTGTCAACGACGACCTTGCCTTACGCTTCCGCTTCCA 379
686 TTCTGTGTGAGGGAAGCTACTTGTGTTGCTGCTTTGCAACTC 732
380 TTGCTGTGTGTAGTAGGCGACGCTGTGCTGTGCTTGAAGCTCTACCTTCAC 426

RESULT 5
BI190568
LOCUS
DEFINITION

215 bp mRNA linear EST 10-JUL-2001
BI190568
1library Fusarium sporotrichioides cDNA clone 12el1fs 5', mRNA
sequence.
BI190568
BI190568.1 GI:14664247
EST.
Fusarium sporotrichioides.
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; microsporitic Hypocreales; Fusarium.
1 (bases 1 to 215)
Ren.O., Tag.A., Peplow.A., Lai.H., Kupfer.C., Peterson.A., Beremand
M. and Roe.B.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

BI190568
BI190568.1
EST.
Fusarium sporotrichioides.
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; microsporitic Hypocreales; Fusarium.
1 (bases 1 to 215)
Ren.O., Tag.A., Peplow.A., Lai.H., Kupfer.C., Peterson.A., Beremand
M. and Roe.B.

COMMENT

Other ESTs: l2ellfs.f1
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry, University of Oklahoma
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Contact Dr. Marian Beremand regarding clone availability. Included
 is the best homolog from a black search of Genbank nr 04-09-01
 363 7e-35 g111701401sp|P45699.PUTATIVE ENDOGLUCANASE TYPE
 KPRCURSOR (EN)
 Seq primer: T3
 High quality sequence stop: 156.
 Location/Qualifiers

FEATURES

source

1. 215
 /organism="Fusarium sporotrichioides"
 /strain="T1 10"
 /db_xref="taxon:5514"
 /clone="l2ellfs"
 /clone_lib="Fusarium sporotrichioides T1 10 overexpressed
 cDNA library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
 ; 3' end of cDNA cloned into XhoI site of pBluescript"
 44 a 61 c 53 g 56 t 1 others

BASE COUNT

Query Match 7.9%; Score 86; DB 13; Length 215;
 Best Local Similarity 65.6%; Pred. No. 6.9e-12;
 Matches 141; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

ORIGIN

481 TACTGGATTGTTGTAACCTTCTTGACGTTGAGCCCGTAAAGCTGACCTCCCT 540
 1 TACTGGACTGCTGACAGCTTCTTGAGAGCGCAAGCTAAAGTCAAGGCCCT 60
 541 GTTGGCTCTGTAAACAGAGTGTAGACTCTGTGATTAACAACACTCAAAACGGCTGT 600
 61 GCTGTGACTTGTGACAAACAAAGATACCTTACTACTAAGCGTGTGCAAGCGTTGT 120
 601 ---GTTGTGTAGACGAGTACACCTGTATATGACCAACTCAACTTGGTTTGAAGGACAG 657
 121 GAGGAGTGTGTTCTGCTTATGCTGACCAACTCTCCCGTGGCTGTCAAGCAGAC 180
 658 CTTCCTAGCGTTTCCCGCTGCTCCATTCTGG 692
 181 CTGCTTACCGTTTCTGCTCTACCAACTTGTCTGG 215

RESULT 6
 PR0047601 619 bp DNA linear GSS 05-JAN-2001
 LOCUS Fugu rubripes GSS sequence, clone 217A131G11, genomic survey
 DEFINITION

AL444386
 AL444386.1 GI:12052222
 GSS: genome survey sequence.
 KEYWORDS
 SOURCE Takifugu rubripes.
 ORGANISM

REFERENCE
 AUTHORS Clark, M.S.
 TITLE Direct Submission
 JOURNAL Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource
 Centre Hinxton, Cambridge, CB10 1SB, UK Email:
 biohelp@hgm.mrc.ac.uk
 COMMENT Vector: pBluescript II KS
 V type: phagemid
 PRIMER: KS
 DESCR:

FEATURES

source

1. 619
 /organism="Takifugu rubripes"
 /db_xref="taxon:31033"
 /clone="217A131G11"
 /clone_lib="BAC 217A13"
 102 a 172 c 92 g 177 t 76 others

BASE COUNT

Query Match 7.9%; Score 85.6; DB 17; Length 619;
 Best Local Similarity 48.3%; Pred. No. 1.6e-11;
 Matches 190; Conservative 0; Mismatches 203; Indels 0; Gaps 0;

ORIGIN

193 AATGAACCTCAGCTCCAGTCAACAAATCTTTCACAAAACCACTACTAGAGAGTCC 252
 7 ACTGACAGCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 66
 253 AAGAGACTACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 312
 67 ACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 126
 313 ACCACACTACTAGAGCTTCCAGAGACCACTACTACTAGAGCTTAAAGACACAC 372
 127 GCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 186
 373 ACTACTACTAGAGAGCTTCTACTACTACTACTACTACTACTACTACTACTACTACTACT 432
 187 ACT 246
 433 TACTCCGCTCTCTGT 492
 247 AATCTACTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 306
 493 TGTAGCTTCTTGTAGT 552
 307 ACTACTGT 366
 553 AACCAAGATGTAGACTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 585
 367 ACTAGCTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 399

RESULT 7
 CNS02HA4 989 bp DNA linear GSS 13-MAY-2000
 LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
 DEFINITION 139021 of library G from Tetraodon nigroviridis, genomic survey
 sequence.

ACCESSION
 AL197365
 AL197365.1 GI:7835515
 GSS: genome survey sequence.
 KEYWORDS
 SOURCE Tetraodon nigroviridis.
 ORGANISM

REFERENCE
 AUTHORS Bernot, A., Fizames, C., Wincker, P., Brothier, P., Queller, F.,
 Saunin, W., and Weissendbach, J.
 TITLE Human gene number estimate provided by genome wide analysis using
 Tetraodon nigroviridis DNA sequence
 JOURNAL Unpublished
 REFERENCE
 AUTHORS Bernot, A., Fizames, C., Wincker, P., Brothier, P., Queller, F.,
 Saunin, W., and Weissendbach, J.
 TITLE Human gene number estimate provided by genome wide analysis using
 Tetraodon nigroviridis DNA sequence
 JOURNAL Unpublished
 REFERENCE
 AUTHORS Bernot, A., Fizames, C., Wincker, P., Brothier, P., Queller, F.,
 Saunin, W., and Weissendbach, J.
 TITLE Human gene number estimate provided by genome wide analysis using
 Tetraodon nigroviridis DNA sequence
 JOURNAL Unpublished

COMMENT Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 989)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2000)
 COMMENT This sequence is a single read and was generated as part of a large scale clone-and-sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

FEATURES
 source
 1. 989
 /organism="Tetraodon nigroviridis"
 /db_xref="taxon:99883"
 /clone="139021"
 /clone_lib="G"
 /note="Genoscope sequence ID : COAG139AH1LP1-end : 17"

BASE COUNT 320 a 245 c 122 g 261 t 41 others

ORIGIN

Query Match 7.8%; Score 84; DB 17; Length 989;
 Best Local Similarity 50.3%; Pred. No. 5.3e-11;
 Matches 190; Conservative 3; Mismatches 185; Indels 0; Gaps 0;

QY 209 CCACTAACAAATCTTCTCAGAAAACACCACTAGAGTGCAGAGAGACTACCACTA 268
 |||||
 DB 157 CTACTACTAATACTACTAATATCTACTACTAATATCTACTACTAATATCTACTACTA 216
 |||||
 QY 269 CTAAAGTTCAGAGAACCAACCACTAGAGTGCAGAGAGACTACCACTAGAG 328
 |||||
 DB 217 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 276
 |||||
 QY 329 CTTCAGAGAGAACCAACCACTAGAGTGCAGAGAGACTACCACTACTAGAGAG 388
 |||||
 DB 277 CTACTACTAATACTACTAATATCTACTACTACTACTACTACTACTACTACTACTCTG 336
 |||||
 QY 389 CTTCACCTGCACCTG 448
 |||||
 DB 337 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 396
 |||||
 QY 449 GTGTGCTCCGAGTAATGTAAGAACCACTAGAGTGCAGAGAGTGTGTAAGCTCTCTGCA 508
 |||||
 DB 397 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 456
 |||||
 QY 509 GTTGGCCCGTAAAGCTGATGTCACCTCCCTGTTGGCTCCTTAAGAGAGTGTAGA 568
 |||||
 DB 457 NTNGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 516
 |||||
 QY 569 CTCTTGCTGATACACCA 586
 |||||
 DB 517 ATATATCTACTACTCTCCCA 534
 |||||

RESULT 8
 CNS04NSM 735 bp DNA linear GSS 21-MAY-2000
 LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
 DEFINITION 123M05 of library G from Tetraodon nigroviridis, genomic survey
 sequence.
 ACCESSION AL299119 GI:8038260
 VERSION AL299119.1
 KEYWORDS GSS: genome survey sequence.
 SOURCE Tetraodon nigroviridis.
 ORGANISM Tetraodon nigroviridis.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodon.
 1 (bases 1 to 735)
 Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fitzames,C., Wincker,P., Brothier,P., Quetier,F.,
 Saurin,W. and Weissbach,J.
 Human gene number estimate provided by genome wide analysis using
 Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 735)
 AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fitzames,C., Fisher,C.,
 Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
 Weissbach,J.
 TITLE Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 735)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2000)
 COMMENT This sequence is a single read and was generated as part of a large scale clone-and-sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

FEATURES
 source
 1. 735
 /organism="Tetraodon nigroviridis"
 /db_xref="taxon:99883"
 /clone="123M05"
 /clone_lib="G"
 /note="Genoscope sequence ID : COBG123AG03LP1-end : 17"

BASE COUNT 242 a 45 c 223 g 197 t 28 others

ORIGIN

Query Match 7.5%; Score 81.6; DB 17; Length 735;
 Best Local Similarity 59.0%; Pred. No. 1.9e-10;
 Matches 138; Conservative 1; Mismatches 95; Indels 0; Gaps 0;

QY 205 ACCCTCACTAACAAATCTTCTCAGAAAACCACTAGAGTGCAGAGAGACTACCACTACC 264
 |||||
 DB 319 ACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 260
 |||||
 QY 265 ACTACTAAGGTTCCAGAGAACCAACCACTAGAGTGCAGAGAGCTTAAAGAACCACTACT 324
 |||||
 DB 259 ACT 200
 |||||
 QY 325 GAAGCTTCCAGAGAACCAACCACTAGAGTGCAGAGAGCTTAAAGAACCACTACTACTAG 384
 |||||
 DB 199 ACT 140
 |||||
 QY 385 AAGCTTCTACTACTACTACTC 438
 |||||
 DB 139 ACT 86
 |||||

RESULT 9
 BH881398 331 bp DNA linear GSS 05-AUG-2002
 LOCUS hv25c11.b1 WGS-Zmay9f (JM107 adapted methyl filtered) Zea mays
 DEFINITION genomic clone hv25c11 5', DNA sequence.
 ACCESSION BH881398
 VERSION BH881398.1 GI:22117295
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 331)
 Rabinowicz,P.D., O'Shaughnessy,A.L., Ballia,V., Debia,N.,
 Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
 Zuberavert,T., McCombie,W.R. and Martienssen,K.A.
 Genomic shotgun sequences from Zea mays (methyl-filtered)
 Unpublished (2002)
 Contact: W. Richard McCombie
 Iltis Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org

Plate: hv25 row: c column: 11
 Seq primer: -21M3UnivFwd
 Class: Shotgun
 High quality sequence stop: 331.
 Location/Qualifiers

FEATURES

source

1..331
 /organism="Zea mays"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone="hv25c11"
 /lab_host="JM107 or DH5a"
 /note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
 The vector was digested with XbaI and one nucleotide was
 added by fill in in the recessive 3' end. The genomic DNA
 was nebulized, end repaired, adaptor ligated and size
 fractionated using sephadex. The resulting fragments were
 between 0.8 and 3 kb and were cloned into the vector
 l.x/y reads in M13mp19. b/g reads in pUC19. The same
 ligation was transformed in either JM107 or DH5a."
 BASE COUNT
 ORIGIN
 110 a 108 c 6 g 107 t

Query Match
 Best Local Similarity 58.5%; Pred. No. 6.7e-10;
 Matches 137; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 205 ACCTCACTACAAATCTTCTGACAAACCACTGAGAGTCCAGAAAGACTAC 264
 DB 15 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 74
 QY 265 ACTACTAAAGGTTCCAAAGAACCACTGAGAGTCCAGAAAGACTACT 324
 DB 75 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 134
 QY 325 GAAGCTCCAGAGAACCACTGAGAGTCCAGAAAGACTACTACTACTACTACT 384
 DB 135 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 194
 QY 385 AAGGCTTACCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 438
 DB 195 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 248

RESULT 10
 AZ204694 933 bp DNA linear GSS 31-AUG-2000
 LOCUS
 DEFINITION SP 0100_A1 G12 SP68 Strongylocentrotus purpuratus, purple sea
 urchin, sperm genomic BAC library Strongylocentrotus purpuratus
 genomic clone Plate-100 Col-23 Row=M, DNA sequence.
 AZ204694
 VERSION AZ204694.1 GI:8399614
 KEYWORDS
 SOURCE
 ORGANISM
 GSS.
 Strongylocentrotus purpuratus.
 Strongylocentrotus purpuratus
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinoidea; Echinoidea; Echinacea; Echinoida;
 Strongylocentrotidae; Strongylocentrotus.
 1 (bases 1 to 933)

REFERENCE
 AUTHORS
 Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R.,
 Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray,
 G.A., Eitelsohn, C.A., Leinrich, H., Britten, R.J., Davidson, E.H. and
 Hood, L.
 A sea urchin genome project: Sequence scan, virtual map, and
 additional resources
 Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)

JOURNAL
 MEDLINE
 COMMENT
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 California Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047

Email: acameron@caltech.edu
 Plate: 100 row: M column: 23
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 933.
 Location/Qualifiers

FEATURES

source

1..933
 /organism="Strongylocentrotus purpuratus"
 /db_xref="taxon:7668"
 /clone="Plate=100 Col=23 Row=M"
 /clone.lib="Strongylocentrotus purpuratus, purple sea
 urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BAC63.6; BAC Clones in E-Coli
 DH10B"
 BASE COUNT
 ORIGIN
 226 a 235 c 156 g 316 t

Query Match
 Best Local Similarity 57.9%; Pred. No. 1.2e-09;
 Matches 140; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 189 TCCCATGAAACCTCACTCAATCTTCTGACAAACCACTACTGAGAG 248
 DB 209 TACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 268
 QY 249 TGGCAAGAGACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 308
 DB 269 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 328
 QY 309 GAAGACCACTACTGAGAGTCCAGAAAGCACTACTGAGAGTCCAGAAAGAC 368
 DB 329 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 388
 QY 369 CAGCACTACTACTGAGAGTCCAGAGTCTCACTCTCTCTCTCTCTCTCTCTCT 428
 DB 389 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 448
 QY 429 AA 430
 DB 449 TA 450

RESULT 11
 BH879665 350 bp DNA linear GSS 05-AUG-2002
 LOCUS
 DEFINITION ht47h12.g1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
 genomic clone ht47h12 5', DNA sequence.
 BH879665
 VERSION BH879665.1 GI:22115562
 KEYWORDS
 SOURCE
 ORGANISM
 GSS.
 Zea mays.
 Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 350)

REFERENCE
 AUTHORS
 Rabnowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N.,
 Katzenburger, F., King, L., Miller, B., Muller, S., Masciameo, L.,
 Zuber, R., McCombie, W.R. and Marienissen, R.A.
 Genomic shotgun sequences from Zea mays (methyl-filtered)
 Unpublished (2002)
 Contact: W. Richard McCombie
 Cold Spring Harbor Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org

JOURNAL
 MEDLINE
 COMMENT
 Contact: Cameron, RA, Davidson, EH, Hood, L
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 California Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 High quality sequence stop: 350.
 Location/Qualifiers

FEATURES

source

1. .350
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ht47h12"
/lab_host="JM107 or DH5a"
/note="Organ: Immature ears; Site 1: Xba I; Site 2: Xba I; The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (x/y reads in M13mp19, b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a."

BASE COUNT 112 a 110 c 13 g 115 t

ORIGIN

Query Match 7.2%; Score 77.8; DB 17; Length 350;
Best Local Similarity 55.3%; Pred. No. 1.3e-09;
Matches 151; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

Qy 205 ACTCCACTACAAATCTTCTCAAAAACCACTACTAGAGTCCAGAGACTACC 264
Db 73 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 132
Qy 265 ACTACTAAAGTTCCAGAGACCACTACTAGAGCTTAAGAGACCACTACT 324
Db 133 ACTACTACTACTACTACTACTACTACTACTACTAGACTACTACTACTACT 192
Qy 325 GAAGCTTCAAGAGACCACTACTAGAGCTTAAGAGACCACTACTACTAG 384
Db 193 GCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 252
Qy 385 AAGGCTTCTACCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 444
Db 253 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 312
Qy 445 TCTGTGTGTCCTCCGATAGTGGAACACT 477
Db 313 ACGGCTACTGCTACTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGT 345

RESULT 12

LOCUS AZ183942 788 bp DNA linear GSS 30-AUG-2000
DEFINITION SP_1002_A1_H11.SP6 Strongylocentrotus purpuratus, purple sea urchin
, sperm genomic BAC library Strongylocentrotus purpuratus genomic
clone Plate=1002 Col=21 Row=O, DNA sequence.

ACCESSION AZ183942
VERSION AZ183942.1 GI:8356317
KEYWORDS GSS.
SOURCE Strongylocentrotus purpuratus.
ORGANISM Strongylocentrotus purpuratus.
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Echinoidea; Echinacea; Echinoda;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 788)
Cameron,R.A., Mahaitas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
Swartzell,S., Wallace,J.C., Pousetka,A.J., Livingston,B.T., Wray,
G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and
Hood,L.
A sea urchin genome project: Sequence scan, virtual map, and
additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)

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COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L
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California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu

Plate: 1002 row: 0 column: 21
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 788.
Location/Qualifiers

FEATURES

source

1. .788
/organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
/clone="plate=1002 Col=21 Row=O"
/note="Organ: sperm genomic BAC library"
/note="Organ: sperm; Vector: BACs 3.6; BAC clones in E-Coli
DH10B"

BASE COUNT 248 a 183 c 98 g 259 t

ORIGIN

Query Match 7.2%; Score 77.8; DB 17; Length 788;
Best Local Similarity 60.8%; Pred. No. 2e-09;
Matches 127; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 221 CTTCCTCAAAAACCACTACTAGAGTCCAGAGACTACTACTAAAGTTCCA 280
Db 325 CTTCCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 384
Qy 281 AGAAGACCACTACTAGAGCTCTAAGAGACCACTACTAGAGCTTCAAGA 340
Db 385 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 444
Qy 341 CCACCACTACTAGAGCTCTAAGAGACCACTACTACTAGAGCTTCAAGTCCA 400
Db 445 CCACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 504
Qy 401 CTTCCTCA 429
Db 505 TTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 533

RESULT 13

LOCUS AZ205202 914 bp DNA linear GSS 31-AUG-2000
DEFINITION SP_0100_A2_G12.SP6 Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library Strongylocentrotus purpuratus
genomic clone Plate=100 Col=24 Row=W, DNA sequence.

ACCESSION AZ205202
VERSION AZ205202.1 GI:8400122
KEYWORDS GSS.
SOURCE Strongylocentrotus purpuratus.
ORGANISM Strongylocentrotus purpuratus.
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Echinoidea; Echinacea; Echinoda;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 914)
Cameron,R.A., Mahaitas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
Swartzell,S., Wallace,J.C., Pousetka,A.J., Livingston,B.T., Wray,
G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and
Hood,L.
A sea urchin genome project: Sequence scan, virtual map, and
additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)

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COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 914.
Location/Qualifiers

FEATURES

source

1. .914

Wed Jun 18 17:56:02 2003

us-09-807-933b-6.rst

Page 8

/organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
/clone="Plate=100 Col=24 Row=M"
/clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
/note="Organ: Sperm; Vector: BACs 6; BAC clones in E-Coli DH10B"

BASE COUNT 210 a 208 c 107 g 387 t 2 others

ORIGIN

Query Match
Best Local Similarity 7.2%; Score 77.8; DB 17; Length 914;
Matches 157; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 205 ACCCTCACTAACAATCTTCCACAAACCACTACTAGAGTGCAGAAAGCTACC 264
DB 202 ACTACTCTACACACTACTACTATTTACTACACCACTACTACTCTGCACACTACTACT 261
QY 265 ACTACTAAGGCTCCAGAACCACTACTAGAGTGCAGAAAGCTACTACTACT 261
DB 262 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 321
QY 325 GAAGCTCCAGAACCACTACTAGAGTGCAGAAAGCTACTACTACTACTACTACT 321
DB 322 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 384
QY 385 AAGGCTCTACCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 381
DB 382 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 444
QY 445 TCTGTGTGTCCTCCGCTGATGATGATGATGATGATGATGATGATGATGATGAT 493
DB 442 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 490

RESULT 14
FR0048073 494 bp DNA linear GSS 05-JAN-2001
LOCUS Fugu rubripes GSS sequence, clone 263K15bD8, genomic survey
DEFINITION
ACCESSION AL444858
VERSION AL444858.1 GI:12052694
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes.
ORGANISM Takifugu rubripes.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
Tetraodontidae; Takifugu.
1 (bases 1 to 494)
Clark, M.S.
Direct Submission
Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB, UK Email:
biohelp@hmp.mrc.ac.uk
Vector: pBluescript II KS
V-type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of BAC (pBelobACII) cloned
genomic sequence
The BACs can be obtained from <http://www.incyte.com>.

FEATURES
source
1..494
Location/Qualifiers
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone="263K15bD8"
/clone_lib="BAC 263K15"
128 a 163 c 45 g 158 t

Query Match
Best Local Similarity 7.2%; Score 77.6; DB 17; Length 494;
Matches 51.1%; Pred. No. 1.7e-09;

Matches 182; Conservative 0; Mismatches 174; Indels 0; Gaps 0;
QY 233 CCACCACTACGAGAGGCGCAAGAAAGTACACTACTAAAGTTCAGAAAGCAACA 292
DB 124 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 183
QY 293 CTACTGAGGCTCTAAGAAAGCAACAAGTACACTACTAAAGTTCAGAAAGCAACA 352
DB 184 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 243
QY 353 AAGCTCTAAGAAAGCAACAAGTACACTACTAAAGTTCAGAAAGTTCAGAAAGT 412
DB 244 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 472
QY 413 CTCTTTCTGCTTCAAAAGTACCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 472
DB 304 CTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 472
QY 473 CCACCTGCTACGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 472
DB 364 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 532
QY 533 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423
DB 424 CTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479

RESULT 15
B1187393 299 bp mRNA linear EST 10-JUN-2001
LOCUS B1187393
DEFINITION B1187393.1 GI:14661072
ACCESSION B1187393
VERSION B1187393.1
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Microsporici Hypocreales; Fusarium.
1 (bases 1 to 299)
Ren, O., Tag, B., Peplow, A., Lai, H., Kuyfer, C., Peterson, A., Beremand
Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Contact: Bruce A. Roe, University of Oklahoma, broeou@ou.edu
Department of Chemistry and Biochemistry
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broeou@ou.edu
Contact: Dr. Marian Beremand regarding clone availability. Included
is the best homolog from a blastx search of Genbank nr 04-09-01
326, le-30 g11170140/sp145659 FURATIVE ENDONUCLEASE TYPE
KRECKROR (EN
Seq primer: T3
High quality sequence stop: 289.
Location/Qualifiers
1..299
Location/Qualifiers
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="a3b03fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
SmaI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"

FEATURES
source
1..299
Location/Qualifiers
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="a3b03fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
SmaI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 65 a 84 c 54 g 96 t

Query Match 7.1%; Score 76.4; DB 13; Length 299;
Best Local Similarity 67.7%; Pred. No. 2.7e-09;
Matches 107; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy	449	GTGTCCTCCGATATGATGAAACCACTCGCTACTGGATTTGTATAGCTTCTTGCA	508
Db	142	GTGTCCTCTTGGAGAGTGGCCACTCTACTGATCTGGACTGCGAAGCCTTCTTGT	201
Qy	509	GTTGCCCCGATAGGCTGATGTCACTCCCTGTTGGCTCCTGTAAACAAGATGTAGA	568
Db	202	CTTGAGCGGCAAGGCTAAAGTCAAGCGCCCTGCTGTGACTTGTGACAAACAATACC	261
Qy	569	CTCTTGCTGATTAACAACAACCTCAAAACGGCTGTGTGT	606
Db	262	CTATCACTAACCTGAAGCTGTCAACGGTTGTGAGGGT	299

Search completed: June 17, 2003, 18:49:27
Job time : 1462.69 secs

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